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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,917

DATE: 01/24/2002

TIME: 19:23:38

Input Set : N:\Crf3\RULE60\09899917.raw  
 Output Set: N:\CRF3\01242002\I899917.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: Olsen, Henrik S.  
 6 Ruben, Steven M.  
 8 (ii) TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I  
 10 (iii) NUMBER OF SEQUENCES: 17  
 12 (iv) CORRESPONDENCE ADDRESS:  
 13 (A) ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.  
 14 (B) STREET: 1100 New York Ave., NW, Suite 600  
 15 (C) CITY: Washington  
 16 (D) STATE: DC  
 17 (E) COUNTRY: USA  
 18 (F) ZIP: 20005-3934  
 20 (v) COMPUTER READABLE FORM:  
 21 (A) MEDIUM TYPE: Floppy disk  
 22 (B) COMPUTER: IBM PC compatible  
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
 26 (vi) CURRENT APPLICATION DATA:  
 27 (A) APPLICATION NUMBER: US/09/899,917  
 C--> 28 (B) FILING DATE: 09-Jul-2001  
 C--> 29 (C) CLASSIFICATION:  
 36 (vii) PRIOR APPLICATION DATA:  
 32 (A) APPLICATION NUMBER: 08/994,962  
 33 (B) FILING DATE:  
 37 (A) APPLICATION NUMBER: US 60/037,388  
 38 (B) FILING DATE: 07-FEB-1997  
 41 (viii) ATTORNEY/AGENT INFORMATION:  
 42 (A) NAME: Steffe, Eric K.  
 43 (B) REGISTRATION NUMBER: 36,688  
 44 (C) REFERENCE/DOCKET NUMBER: 1488.0440002  
 46 (ix) TELECOMMUNICATION INFORMATION:  
 47 (A) TELEPHONE: 202-371-2600  
 48 (B) TELEFAX: 202-371-2540  
 51 (2) INFORMATION FOR SEQ ID NO: 1:  
 53 (i) SEQUENCE CHARACTERISTICS:  
 54 (A) LENGTH: 860 base pairs  
 55 (B) TYPE: nucleic acid  
 56 (C) STRANDEDNESS: double  
 57 (D) TOPOLOGY: linear  
 59 (ii) MOLECULE TYPE: cDNA  
 62 (ix) FEATURE:  
 63 (A) NAME/KEY: CDS

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64 (B) LOCATION: 20..505  
66 (ix) FEATURE:  
67 (A) NAME/KEY: sig\_peptide  
68 (B) LOCATION: 20..79  
70 (ix) FEATURE:  
71 (A) NAME/KEY: mat\_peptide  
72 (B) LOCATION: 80..505  
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
77 TCCCCATACAG GCCCCCACC ATG AAG GGT TTC ACA GCC ACT CTC TTC CTC TGG 52  
78 Met Lys Gly Phe Thr Ala Thr Leu Phe Leu Trp  
79 -20 -15 -10  
81 ACT CTG ATT TTT CCC AGC TGC AGT GGA GGC GGC GGT GGG AAA GCC TGG 100  
82 Thr Leu Ile Phe Pro Ser Cys Ser Gly Gly Gly Gly Lys Ala Trp  
83 -5 1 5  
85 CCC ACA CAC GTG GTC TGT AGC GAC AGC GGC TTG GAA GTG CTC TAC CAG 148  
86 Pro Thr His Val Val Cys Ser Asp Ser Gly Leu Glu Val Leu Tyr Gln  
87 10 15 20  
89 AGT TGC GAT CCA TTA CAA GAT TTT GGC TTT TCT GTT GAA AAG TGT TCC 196  
90 Ser Cys Asp Pro Leu Gln Asp Phe Gly Phe Ser Val Glu Lys Cys Ser  
91 25 30 35  
93 AAG CAA TTA AAA TCA AAT ATC AAC ATT AGA TTT GGA ATT ATT CTG AGA 244  
94 Lys Gln Leu Lys Ser Asn Ile Asn Ile Arg Phe Gly Ile Ile Leu Arg  
95 40 45 50 55  
97 GAG GAC ATC AAA GAG CTT TTT CTT GAC CTA GCT CTC ATG TCT CAA GGC 292  
98 Glu Asp Ile Lys Glu Leu Phe Leu Asp Leu Ala Leu Met Ser Gln Gly  
99 60 65 70  
101 TCA TCT GTT TTG AAT TTC TCC TAT CCC ATC TGT GAG GCG GCT CTG CCC 340  
102 Ser Ser Val Leu Asn Phe Ser Tyr Pro Ile Cys Glu Ala Ala Leu Pro  
103 75 80 85  
105 AAG TTT TCT TTC TGT GGA AGA AGG AAA GGA GAG CAG ATT TAC TAT GCT 388  
106 Lys Phe Ser Phe Cys Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala  
107 90 95 100  
109 GGG CCT GTC AAT AAT CCT GAA TTT ACT ATT CCT CAG GGA GAA TAC CAG 436  
110 Gly Pro Val Asn Asn Pro Glu Phe Thr Ile Pro Gln Gly Glu Tyr Gln  
111 105 110 115  
113 GTT TTG CTG GAA CTG TAC ACT GAA AAA CGG TCC ACC GTG GCC TGT GCC 484  
114 Val Leu Leu Glu Leu Tyr Thr Glu Lys Arg Ser Thr Val Ala Cys Ala  
115 120 125 130 135  
117 AAT GCT ACT ATC ATG TGC TCC TGACTGTGGC CTGTAGCAAA AATCACAGCC 535  
118 Asn Ala Thr Ile Met Cys Ser  
119 140  
121 AGCTGCATCT CGTGGGACCT CCAAGCTCCT CTGACTGAAC CTACTGTGGG AGGAGAAGCA 595  
123 GCTGATGACA GAGAGAGGCT CTACAAAGAA GCGCCCCAA AGAGTGCAGC TGCTAATT 655  
125 AGTCCCAGGA CCAGACATCC CCAGACTCCA CAGATGTAAT GAAGTCCCCG AATGTATCTG 715  
127 TTTCTAAGGA GCCTCTTGGC AGTCCTTAAG CAGTCTTGAG GGTCCATCCT TTTCTCTAA 775  
129 TTGGTCGCCT CCCACCAAGAC TCACCTGCTT TTCAACTTT TAGGAGTGCT TCCTCACAGT 835  
131 TACCAAGAAA TAAAGAAAGC TGGCC 860  
134 (2) INFORMATION FOR SEQ ID NO: 2:  
136 (i) SEQUENCE CHARACTERISTICS:

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137 (A) LENGTH: 162 amino acids  
 138 (B) TYPE: amino acid  
 139 (D) TOPOLOGY: linear  
 141 (ii) MOLECULE TYPE: protein  
 143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 145 Met Lys Gly Phe Thr Ala Thr Leu Phe Leu Trp Thr Leu Ile Phe Pro  
 146 -20 -15 -10 -5  
 148 Ser Cys Ser Gly Gly Gly Gly Lys Ala Trp Pro Thr His Val Val  
 149 1 5 10  
 151 Cys Ser Asp Ser Gly Leu Glu Val Leu Tyr Gln Ser Cys Asp Pro Leu  
 152 15 20 25  
 154 Gln Asp Phe Gly Phe Ser Val Glu Lys Cys Ser Lys Gln Leu Lys Ser  
 155 30 35 40  
 157 Asn Ile Asn Ile Arg Phe Gly Ile Ile Leu Arg Glu Asp Ile Lys Glu  
 158 45 50 55 60  
 160 Leu Phe Leu Asp Leu Ala Leu Met Ser Gln Gly Ser Ser Val Leu Asn  
 161 65 70 75  
 163 Phe Ser Tyr Pro Ile Cys Glu Ala Ala Leu Pro Lys Phe Ser Phe Cys  
 164 80 85 90  
 166 Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala Gly Pro Val Asn Asn  
 167 95 100 105  
 169 Pro Glu Phe Thr Ile Pro Gln Gly Glu Tyr Gln Val Leu Leu Glu Leu  
 170 110 115 120  
 172 Tyr Thr Glu Lys Arg Ser Thr Val Ala Cys Ala Asn Ala Thr Ile Met  
 173 125 130 135 140  
 175 Cys Ser  
 178 (2) INFORMATION FOR SEQ ID NO: 3:  
 180 (i) SEQUENCE CHARACTERISTICS:  
 181 (A) LENGTH: 133 amino acids  
 182 (B) TYPE: amino acid  
 183 (C) STRANDEDNESS: Not Relevant  
 W--> 184 (D) TOPOLOGY: Not Relevant  
 186 (ii) MOLECULE TYPE: protein  
 191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 193 Trp Pro Thr His Thr Val Cys Lys Glu Glu Asn Leu Glu Ile Tyr Tyr  
 194 1 5 10 15  
 196 Lys Ser Cys Asp Pro Gln Gln Asp Phe Ala Phe Ser Ile Asp Arg Cys  
 197 20 25 30  
 199 Ser Asp Val Thr Thr His Thr Phe Asp Ile Arg Ala Ala Met Val Leu  
 200 35 40 45  
 202 Arg Gln Ser Ile Lys Glu Leu Tyr Ala Lys Val Asp Leu Ile Ile Asn  
 203 50 55 60  
 205 Gly Lys Thr Val Leu Ser Tyr Ser Glu Thr Leu Cys Gly Pro Gly Leu  
 206 65 70 75 80  
 208 Ser Lys Leu Ile Phe Cys Gly Lys Lys Gly Glu His Leu Tyr Tyr  
 209 85 90 95  
 211 Glu Gly Pro Ile Thr Leu Gly Ile Lys Glu Ile Pro Gln Gly Asp Tyr  
 212 100 105 110  
 214 Thr Ile Thr Ala Arg Leu Thr Asn Glu Asp Arg Ala Thr Val Ala Cys

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215	115	120	125	
217	Ala Asp Phe Thr Val			
218	130			
220	(2) INFORMATION FOR SEQ ID NO: 4:			
222	(i) SEQUENCE CHARACTERISTICS:			
223	(A) LENGTH: 29 base pairs			
224	(B) TYPE: nucleic acid			
225	(C) STRANDEDNESS: single			
226	(D) TOPOLOGY: linear			
228	(ii) MOLECULE TYPE: cDNA			
233	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:			
235	GAATCCATGG GCGGCGGTGG GAAAGCCTG			29
237	(2) INFORMATION FOR SEQ ID NO: 5:			
239	(i) SEQUENCE CHARACTERISTICS:			
240	(A) LENGTH: 30 base pairs			
241	(B) TYPE: nucleic acid			
242	(C) STRANDEDNESS: single			
243	(D) TOPOLOGY: linear			
245	(ii) MOLECULE TYPE: cDNA			
250	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:			
252	GAATGAGATCT GGAGCACATG ATAGTAGCAT			30
254	(2) INFORMATION FOR SEQ ID NO: 6:			
256	(i) SEQUENCE CHARACTERISTICS:			
257	(A) LENGTH: 36 base pairs			
258	(B) TYPE: nucleic acid			
259	(C) STRANDEDNESS: single			
260	(D) TOPOLOGY: linear			
262	(ii) MOLECULE TYPE: cDNA			
267	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:			
269	GAATGGATCC GCCATCATGA AGGGTTTAC AGCCAC			36
271	(2) INFORMATION FOR SEQ ID NO: 7:			
273	(i) SEQUENCE CHARACTERISTICS:			
274	(A) LENGTH: 29 base pairs			
275	(B) TYPE: nucleic acid			
276	(C) STRANDEDNESS: single			
277	(D) TOPOLOGY: linear			
279	(ii) MOLECULE TYPE: cDNA			
284	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:			
286	GAATGGTACC AGCAGCTGCA CTCTTTGGG			29
288	(2) INFORMATION FOR SEQ ID NO: 8:			
290	(i) SEQUENCE CHARACTERISTICS:			
291	(A) LENGTH: 36 base pairs			
292	(B) TYPE: nucleic acid			
293	(C) STRANDEDNESS: single			
294	(D) TOPOLOGY: linear			
296	(ii) MOLECULE TYPE: cDNA			
301	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:			
303	AGCTAAGCTT CCGCCACCAT GAAGGGTTTC ACAGCC			36
305	(2) INFORMATION FOR SEQ ID NO: 9:			

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Input Set : N:\CrF3\RULE60\09899917.raw

Output Set: N:\CRF3\01242002\I899917.raw

307	(i) SEQUENCE CHARACTERISTICS:	
308	(A) LENGTH: 62 base pairs	
309	(B) TYPE: nucleic acid	
310	(C) STRANDEDNESS: single	
311	(D) TOPOLOGY: linear	
313	(ii) MOLECULE TYPE: cDNA	
318	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
320	CAGTCTCGAG TTAAGCGTAG TCTGGGACGT CGTATGGGTA GGAGCACATG ATAGTAGCAT	60
322	TG	62
324	(2) INFORMATION FOR SEQ ID NO: 10:	
326	(i) SEQUENCE CHARACTERISTICS:	
327	(A) LENGTH: 29 base pairs	
328	(B) TYPE: nucleic acid	
329	(C) STRANDEDNESS: single	
330	(D) TOPOLOGY: linear	
332	(ii) MOLECULE TYPE: cDNA	
337	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
339	GACTGGTACC AGCAGCTGCA CTCTTTGGG	29
341	(2) INFORMATION FOR SEQ ID NO: 11:	
343	(i) SEQUENCE CHARACTERISTICS:	
344	(A) LENGTH: 514 base pairs	
345	(B) TYPE: nucleic acid	
346	(C) STRANDEDNESS: double	
347	(D) TOPOLOGY: linear	
349	(ii) MOLECULE TYPE: cDNA	
354	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
356	NAATTTCGCGA GATTTTCCC AGCTGCAGTG GAGGCGCGG TGGGAAAGCC TGGCCCACAC	60
358	ACGTGGTCTG TAGCGACAGG CTTTGGAAAGT GCTCTACCAG AGTTCGCGATC CATTACAAGA	120
360	TTTTGGCTTT TCTGTTGAAA AGTGTTCAGA GCAATTAAAA TCAAATATCA ACATTAGATT	180
362	TGGAATTATT CTGAAGGACA TCAAAGAGCT TTTTCTTGAC CTAGCTCTCA TGTNTCAAGG	240
364	CTCATCTGTT TTGAATTCT CCTATCCCAT CTGTGAGGCG GCTCTGCCAA GTTTCTTTC	300
366	TGTGGAAGAA GGAAAGGAGA GCAGATTAC TATGCTNGGG CTGTCATAAA TNCNGAATTT	360
368	ACTATTCCT CANGGGGAT TACCAAGTT TGCTGGGACT GTACAATGAA AAACGGTCCA	420
370	CCGNGGCNGT GCCATGGTAC TATCGNGTGG TCCGACTGTG GCCNTAGGAA AATCACACCA	480
372	TTGNATTCCG GGNCNCCAGT CCTTGATNAC CNAN	514
374	(2) INFORMATION FOR SEQ ID NO: 12:	
376	(i) SEQUENCE CHARACTERISTICS:	
377	(A) LENGTH: 457 base pairs	
378	(B) TYPE: nucleic acid	
379	(C) STRANDEDNESS: double	
380	(D) TOPOLOGY: linear	
382	(ii) MOLECULE TYPE: cDNA	
387	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
389	CACAGCCACT CTCTTCTCT GGACTCTAAT TTTNCCCAGC TGCAGTGGAG GCGGCGGTGG	60
391	GAAAGCCTGG CCCACACACG TGGTCTGTAG CGACANGGCT TGGAAAGTGCT CTACCAGAGT	120
393	TGCGATCCAT TACAAGATTT TGGCTTTCT GTTGAAAAGT GTTCCAAGCA ATTAAAATCA	180
395	AATATCAACA TTAGATTGAG AATTATTCTG AGAGAGGACA TCAAAGAGCT TTTTCTTGAC	240
397	CTAGCTCTCA TGTCTCAAGG CTCATCTGTT TTNAATTCT CCTATCCCAT CTGTNAGGCG	300
399	GCTCTGCCCA AGTTTCTTT CTGTGGAAGA AGGAAAGGAG AGCAGATTAA CTATGCTGGG	360

**VERIFICATION SUMMARY**

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:184 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3

L:516 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17